

Appendix III

Alignment of instant SEQ ID NO: 1 (nucleotides 770-1310) with HpaI-MroII (314 bp) deletion fragment of Thudium et al

Alignment of nucleotides 1-314 of SEQ ID NO: 1 of Thudium et al with instant SEQ ID NO: 1

Score = 614 bits (680), Expect = 2e-180
Identities = 380/401 (94%), Gaps = 8/401 (1%)
Strand=Plus/Plus

Query	782	GTAAGTACCGCCTATAGAGTCTATAGGCCACCCCTTGGCTTCTTATGCATGCTATACT	841
Sbjct	1	GTAAGTACCGCCTATAGACTCTATAGGCACACCCCTTGGCT-CTTATGCATGCTATACT	59
Query	842	GTTTTTGGCTTGGGGTCTATACACCCCGCTTCCTCATGTTATAGGTGATGGTATAGCTT	901
Sbjct	60	GTTTTTGGCTTGGGGCTATACACCCCGCT-CCTTATGCTATAGGTGATGGTATAGCTT	118
Query	902	AGCCTATAGGTGTGGGTATTGACCATATTGACCACTCCCTATTGGTGACGATACTTT	961
Sbjct	119	AGCCTATAGGTGTGGGTATTGACCATATTGACCACTCCCTATTGGTGACGATACTTT	178
Query	962	CCATTACTAATCCATAACATGGCTCTTTGCCACAACCTCTCTTTATTGGCTATATGCCAAT	1021
Sbjct	179	CCATTACTAATCCATAACATGGCTCTTTGCCACAACCTATCTCTATTGGCTATATGCCAAT	238
Query	1022	ACACTGTCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGATGGGGTCTCATTTAT	1081
Sbjct	239	ACTCTGTCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGATGGGGTC-CATTTAT	297
Query	1082	TATTTACAAATTCACATATACAACACCCGCTCCCGAGTGCCCGCAGTTTTTATTAAACA	1141
Sbjct	298	TATTTACAAATTCACATATACAACACCCGCTCCCGAGTGCCCGCAGTTTTTATTAAACA	357
Query	1142	TAACGTGGGATCTCC-ACGCGAATCTCGGGTACGTGTTCG	1181
Sbjct	358	TACCGTGGGATCTCCGAC----ATCTCGGGTACGTGTTCG	394

Alignment of nucleotides 710-828 of SEQ ID NO: 1 of Thudium et al with instant SEQ ID NO: 1

Score = 220 bits (119), Expect = 2e-62
Identities = 119/119 (100%), Gaps = 0/119 (0%)
Strand=Plus/Plus

Query	1183	AACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGGCCACCAGACA	1242
Sbjct	710	AACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGGCCACCAGACA	769
Query	1243	TAATAGCTGACAGACTAACAGACTGTTCCCTTTCCATGGGTCTTTCTGCAGTCACCGTC	1301
Sbjct	770	TAATAGCTGACAGACTAACAGACTGTTCCCTTTCCATGGGTCTTTCTGCAGTCACCGTC	828